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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Gray, Patrick W.
Schweickart, Vicky L.
Raport, Carol J.

(ii) TITLE OF INVENTION: Chemokine Receptor Materials and Methods

(iii) NUMBER OF SEQUENCES: 20

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
(B) STREET: 6300 Sears Tower, 233 S. Wacker Drive
(C) CITY: Chicago
(D) STATE: Illinois
(E) COUNTRY: USA
(F) ZIP: 60606

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Noland, Greta E.
(B) REGISTRATION NUMBER: 35,302
(C) REFERENCE/DOCKET NUMBER: 27866/33670

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 312-474-6300
(B) TELEFAX: 312-474-0448

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3383 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 55..1110

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION: /= "88C polynucleotide and amino acid
sequences"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGAAGAGCTG AGACATCCGT TCCCCTACAA GAAACTCTCC CGGGGTGGAA CAAG ATG
Met
1

GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC ATC AAT TAT TAT ACA TCG Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr Ser 5	10	15	105
GAG CCC TGC CAA AAA ATC AAT GTG AAG CAA ATC GCA GCC CGC CTC CTG Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu Leu 20	25	30	153
CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT GGT TTT GTG GGC AAC ATG Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met 35	40	45	201
CTG GTC ATC CTC ATC CTG ATA AAC TGC AAA AGG CTG AAG AGC ATG ACT Leu Val Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met Thr 50	55	60	249
GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT GAC CTG TTT TTC CTT CTT Asp Ile Tyr Leu Leu Asn Ala Ile Ser Asp Leu Phe Phe Leu Leu 70	75	80	297
ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC GCC CAG TGG GAC TTT GGA Thr Val Pro Phe Trp Ala His Tyr Ala Ala Gln Trp Asp Phe Gly 85	90	95	345
AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC TTC Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe Phe 100	105	110	393
TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG GCT Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala 115	120	125	441
GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT GGG Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly 130	135	140	489
GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GCT GTG TTT GCG TCT CTC Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser Leu 150	155	160	537
CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC ACC Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr Thr 165	170	175	585
TGC AGC TCT CAT TTT CCA TAC AGT CAG TAT CAA TTC TGG AAG AAT TTC Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn Phe 180	185	190	633
CAG ACA TTA AAG ATA GTC ATC TTG GGG CTG GTC CTG CCG CTG CTT GTC Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu Val 195	200	205	681
ATG GTC ATC TGC TAC TCG GGA ATC CTA AAA ACT CTG CTT CGG TGT CGA Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys Arg 210	215	220	729
AAT GAG AAG AAG AGG CAC AGG GCT GTG AGG CTT ATC TTC ACC ATC ATG Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile Met 230	235	240	777
ATT GTT TAT TTT CTC TTC TGG GCT CCC TAC AAC ATT GTC CTT CTC CTG Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu Leu 245	250	255	825
AAC ACC TTC CAG GAA TTC TTT GGC CTG AAT AAT TGC AGT AGC TCT AAC Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Asn 260	265	270	873

AGG TTG GAC CAA GCT ATG CAG GTG ACA GAG ACT CTT GGG ATG ACG CAC Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr His 275 280 285.	921
TGC TGC ATC AAC CCC ATC ATC TAT GCC TTT GTC GGG GAG AAG TTC AGA Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe Arg 290 295 300 305	969
AAC TAC CTC TTA GTC TTC CAA AAG CAC ATT GCC AAA CGC TTC TGC Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe Cys 310 315 320	1017
AAA TGC TGT TCT ATT TTC CAG CAA GAG GCT CCC GAG CGA GCA AGC TCA Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser Ser 325 330 335	1065
GTT TAC ACC CGA TCC ACT GGG GAG CAG GAA ATA TCT GTG GGC TTG Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu 340 345 350	1110
TGACACGGAC TCAAGTGGGC TGGTGACCCA GTCAGAGTTG TGCACATGGC TTAGTTTCA TACACAGCCT GGGCTGGGG TGCGGTGGGA GAGGTCTTTT TTAAAAGGAA GTTACTGTTA TAGAGGGTCT AAGATTTCATC CATTATTTG GCATCTGTT AAAGTAGATT AGATCTTTA AGCCCATCAA TTATAGAAAG CCAAATCAAATATGTTGAT GAAAAATAGC AACCTTTTA TCTCCCTTC ACATGCATCA AGTTATTGAC AAACCTCTCCC TTCACTCCGA AAGTTCCCTA TGTATATTAA AAAGAAAGCC TCAGAGAATT GCTGATTCTT GAGTTAGTG ATCTGAACAG AAATACCAAA ATTATTCAG AAATGTACAA CTTTTTACCT AGTACAAGGC AACATATAAGG TTGTAAAATGT GTTTAAAACA GGTCTTGTC TTGCTATGGG GAGAAAAGAC ATGAATATGA TTAGTAAAGA AATGACACTT TTCAATGTGTG ATTTCCCTC CAAGGTATGG TTAATAAGTT TCACTGACTT AGAACCCAGGC GAGAGACTTG TGCGCTGGGA GAGCTGGGA AGCTTCTTAA ATGAGAAGGA ATTTGAGTTG GATCATCTAT TGCTGGAAA GACAGAAGCC TCACTGCAAG CACTGCATGG GCAAGCTTGG CTGTAGAAGG AGACAGAGCT GGTTGGGAAG ACATGGGGAG GAAGGACAAG GCTAGATCAT GAAGAACCTT GACGGCATTG CTCCGTCTAA GTCATGAGCT GAGCAGGGAG ATCCTGGTTG GTGTTGCAGA AGGTTTACTC TGTGCCAAA GGAGGGTCAG GAAGGATGAG CATTAGGGC AAGGAGACCA CCAACAGCCC TCAGGTCAGG GTGAGGATGG CCTCTGCTAA GCTCAAGGCG TGAGGATGGG AAGGAGGGAG GTATTCGTAAGG GGATGGGAAG GAGGGAGGTAA TTCTGTCAGC ATATGAGGAT GCAGAGTCAG CAGAACTGGG GTGGATTGAG TTTGGAAAGTG AGGGTCAGAG AGGAGTCAGA GAGAATCCCT AGTCTTCAAG CAGATTGGAG AAACCCCTGA AAAGACATCA AGCACAGAAG GAGGAGGGAGG AGGTTTAGGT CAAGAAGAAG ATGGATTGGT GTAAAAGGAT GGGTCTGGTT TGCGAGAGCTT GAACACAGTC TCACCCAGAC TCCAGGCTGT CTTCACTGA ATGCTTCTGA CTTCATAGAT TTCCCTCCCA TCCCAGCTGA AATACTGAGG GGTCTCCAGG AGGAGACTAG ATTTATGAAT ACACGAGGTAA TGAGGTCTAG GAACATACTT CAGCTCACAC ATGAGATCTA GGTGAGGATT GATTACCTAG TAGTCATTC ATGGGTTGTT GGGAGGATTC TATGAGGCAA CCACAGGCAG CATTAGCAC ATACTACACA	1170 1230 1290 1350 1410 1470 1530 1590 1650 1710 1770 1830 1890 1950 2010 2070 2130 2190 2250 2310 2370 2430 2490 2550

TTCAATAAGC ATCAAACCTCT TAGTTACTCA TTCAGGGATA GCACTGAGCA AAGCATTGAG	2610
CAAAGGGGTC CCATATAGGT GAGGGAAAGCC TGAAAAACTA AGATGCTGCC TGCCCAGTGC	2670
ACACAAGTGT AGGTATCATT TTCTGCATTT AACCGTCAAT AGGCAAAGGG GGGAAAGGGAC	2730
ATATTCACTT GGAAATAAGC TGCCTTGAGC CTTAAAACCC ACAAAAGTAC AATTACCAG	2790
CCTCCGTATT TCAGACTGAA TGGGGTGGG GGGGGCGCCT TAGGTACTTA TTCCAGATGC	2850
CTTCTCCAGA CAAACCAGAA GCAACAGAAA AAATCGTCTC TCCCTCCCTT TGAAATGAAT	2910
ATACCCCTTA GTGTTTGGGT ATATTCACTT CAAAGGGAGA GAGAGAGGTT TTTTTCTGTT	2970
CTTTCTCATA TGATTGTGCA CATACTTGAG ACTGTTTGA ATTTGGGGGA TGGCTAAAAC	3030
CATCATAGTA CAGGTAAGGT GAGGAATAG TAAGTGGTGA GAACTACTCA GGGATGAAG	3090
GTGTCAGAAT AATAAGAGGT GCTACTGACT TTCTCAGCCT CTGAATATGA ACGGTGAGCA	3150
TTGTGGCTGT CAGCAGGAAG CAACGAAGGG AAATGTCTTT CCTTTGCTC TTAAGTTGTG	3210
GAGAGTGCAA CAGTAGCATA GGACCCTACC CTCTGGGCCA AGTCAAAGAC ATTCTGACAT	3270
CTTAGTATT GCATATTCTT ATGTATGTGA AAGTTACAAA TTGCTGAAA GAAAATATGC	3330
ATCTAATAAA AAACACCTTC TAAAATAAA AAAAAAAAAA AAAAAAAAAA AAA	3383

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 352 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION: /= "88C amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
1 5 10 15

Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
20 25 30

Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
35 40 45

Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
50 55 60

Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
65 70 75 80

Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
85 90 95

Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
100 105 110

Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
115 120 125

Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
130 135 140

Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
145 150 155 160

Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
165 170 175

Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
180 185 190

Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu
195 200 205

Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
210 215 220

Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
225 230 235 240

Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu
245 250 255

Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser
260 265 270

Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
275 280 285

His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
290 295 300

Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
305 310 315 320

Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
325 330 335

Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu
340 345 350

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 362..1426

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: /= "88-2B polynucleotide and amino acid sequences"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATAATAATGA TTATTATATT GTTATCATTA TCTAGCCTGT TTTTCCTGT TTTGTATTTC 60
TTCCTTAAA TGCTTCAGA AATCTGTATC CCCATTCTTC ACCACCACCC CACAACATTT 120

CTGCTTCTTT TCCCCATGCCG GGTCATGCTA ACTTTGAAAG CTTCAGCTCT TTCCCTCCCTC	180
AATCCTTTTC CTGGCACCTC TGATATGCCT TTTGAAATTCA ATGTTAAAGA ATCCCTAGGC	240
TGCTATCACAC TGTGGCATCT TTGTTGAGTA CATGAATAAA TCAACTGGTG TGTTTTACGA	300
AGGATGATTA TGCTTCATTG TGGGATTGTA TTTTCTTCT TCTATCACAG GGAGAAAGTGA	360
A ATG ACA ACC TCA CTA GAT ACA GTT GAG ACC TTT GGT ACC ACA TCC Met Thr Thr Ser Leu Asp Thr Val Glu Thr Phe Gly Thr Thr Ser	406
1 5 10 15	
TAC TAT GAT GAC GTG GGC CTG CTC TGT GAA AAA GCT GAT ACC AGA GCA Tyr Tyr Asp Asp Val Gly Leu Leu Cys Glu Lys Ala Asp Thr Arg Ala	454
20 25 30	
CTG ATG GCC CAG TTT GTG CCC CCG CTG TAC TCC CTG GTG TTC ACT GTG Leu Met Ala Gln Phe Val Pro Pro Leu Tyr Ser Leu Val Phe Thr Val	502
35 40 45	
GGC CTC TTG GGC AAT GTG GTG GTG ATG ATC CTC ATA AAA TAC AGG Gly Leu Leu Gly Asn Val Val Val Met Ile Leu Ile Lys Tyr Arg	550
50 55 60	
AGG CTC CGA ATT ATG ACC AAC ATC TAC CTG CTC AAC CTG GCC ATT TCG Arg Leu Arg Ile Met Thr Asn Ile Tyr Leu Leu Asn Leu Ala Ile Ser	598
65 70 75	
GAC CTG CTC TTC CTC GTC ACC CTT CCA TTC TGG ATC CAC TAT GTC AGG Asp Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ile His Tyr Val Arg	646
80 85 90 95	
GGG CAT AAC TGG GTT TTT GGC CAT GGC ATG TGT AAG CTC CTC TCA GGG Gly His Asn Trp Val Phe Gly His Gly Met Cys Lys Leu Leu Ser Gly	694
100 105 110	
TTT TAT CAC ACA GGC TTG TAC AGC GAG ATC TTT TTC ATA ATC CTG CTG Phe Tyr His Thr Gly Leu Tyr Ser Glu Ile Phe Ile Ile Leu Leu	742
115 120 125	
ACA ATC GAC AGG TAC CTG GCC ATT GTC CAT GCT GTG TTT GCC CTT CGA Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg	790
130 135 140	
GCC CGG ACT GTC ACT TTT GGT GTC ATC ACC AGC ATC GTC ACC TGG GGC Ala Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Val Thr Trp Gly	838
145 150 155	
CTG GCA GTG CTA GCA GCT CTT CCT GAA TTT ATC TTC TAT GAG ACT GAA Leu Ala Val Leu Ala Ala Leu Pro Glu Phe Ile Phe Tyr Glu Thr Glu	886
160 165 170 175	
GAG TTG TTT GAA GAG ACT CTT TGC AGT GCT CTT TAC CCA GAG GAT ACA Glu Leu Phe Glu Glu Thr Leu Cys Ser Ala Leu Tyr Pro Glu Asp Thr	934
180 185 190	
GTA TAT AGC TGG AGG CAT TTC CAC ACT CTG AGA ATG ACC ATC TTC TGT Val Tyr Ser Trp Arg His Phe His Thr Leu Arg Met Thr Ile Phe Cys	982
195 200 205	
CTC GTT CTC CCT CTG CTC GTT ATG GCC ATC TGC TAC ACA GGA ATC ATC Leu Val Leu Pro Leu Leu Val Met Ala Ile Cys Tyr Thr Gly Ile Ile	1030
210 215 220	
AAA ACG CTG CTG AGG TGC CCC AGT AAA AAA AAG TAC AAG GGC ATC CGG Lys Thr Leu Leu Arg Cys Pro Ser Lys Lys Lys Tyr Lys Ala Ile Arg	1078
225 230 235	

CTC ATT TTT GTC ATC ATG GCG GTG TTT TTC ATT TTC TGG ACA CCC TAC Leu Ile Phe Val Ile Met Ala Val Phe Phe Ile Phe Trp Thr Pro Tyr 240 245 250 255	1126
AAT GTG GCT ATC CTT CTC TCT TCC TAT CAA TCC ATC TTA TTT GGA AAT Asn Val Ala Ile Leu Leu Ser Ser Tyr Gln Ser Ile Leu Phe Gly Asn 260 265 270	1174
GAC TGT GAG CGG AGC AAG CAT CTG GAC CTG GTC ATG CTG GTG ACA GAG Asp Cys Glu Arg Ser Lys His Leu Asp Leu Val Met Leu Val Thr Glu 275 280 285	1222
GTG ATC GCC TAC TCC CAC TGC TGC ATG AAC CCG GTG ATC TAC GCC TTT Val Ile Ala Tyr Ser His Cys Cys Met Asn Pro Val Ile Tyr Ala Phe 290 295 300	1270
GTT GGA GAG AGG TTC CGG AAG TAC CTG CGC CAC TTC TTC CAC AGG CAC Val Gly Glu Arg Phe Arg Lys Tyr Leu Arg His Phe Phe His Arg His 305 310 315	1318
TTG CTC ATG CAC CTG GGC AGA TAC ATC CCA TTC CTT CCT AGT GAG AAG Leu Leu Met His Leu Gly Arg Tyr Ile Pro Phe Leu Pro Ser Glu Lys 320 325 330 335	1366
CTG GAA AGA ACC AGC TCT GTC TCT CCA TCC ACA GCA GAG CCG GAA CTC Leu Glu Arg Thr Ser Ser Val Ser Pro Ser Thr Ala Glu Pro Glu Leu 340 345 350	1414
TCT ATT GTG TTT TAGGTCAGAT GCAGAAAATT GCCTAAAGAG GAAGGACCAA Ser Ile Val Phe 355	1466
GGAGATGAAG CAAACACATT AAGCCTTCCA CACTCACCTC TAAAACAGTC CTTCAAACCTT CCAGTGCAAC ACTGAAGCTC TTGAAGACAC TGAAATATAAC ACACAGCAGT AGCAGTAGAT GCATGTACCC TAAGGTCAATT ACCACAGGCC AGGGGCTGGG CAGCGTACTC ATCATCAACC CTAAAAAGCA GAGCTTGCT TCTCTCTCA AAATGAGTTA CCTACATTTT AATGCACCTG AATGTTAGAT AGTTACTATA TGCCGCTACA AAAAGGTAAA ACTTTTATA TTTTATACAT TAACTTCAGC CAGCTATTGA TATAAATAAA ACATTTCAC ACAATACAAT AAGTTAACTA TTTTATTTTC TAATGTGCCT AGTTCTTCC CTGCTTAATG AAAAGCTTGT TTTTTCAGTG TGAATAAATA ATCGTAAGCA ACAAAAAAA	1526 1586 1646 1706 1766 1826 1886 1915

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 355 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION: /= "88-2B amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Thr Thr Ser Leu Asp Thr Val Glu Thr Phe Gly Thr Thr Ser Tyr 1 5 10 15
--

Tyr Asp Asp Val Gly Leu Leu Cys Glu Lys Ala Asp Thr Arg Ala Leu
20 25 30

Met Ala Gln Phe Val Pro Pro Leu Tyr Ser Leu Val Phe Thr Val Gly
35 40 45

Leu Leu Gly Asn Val Val Val Met Ile Leu Ile Lys Tyr Arg Arg
50 55 60

Leu Arg Ile Met Thr Asn Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
65 70 75 80

Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ile His Tyr Val Arg Gly
85 90 95

His Asn Trp Val Phe Gly His Gly Met Cys Lys Leu Leu Ser Gly Phe
100 105 110

Tyr His Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr
115 120 125

Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala
130 135 140

Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Val Thr Trp Gly Leu
145 150 155 160

Ala Val Leu Ala Ala Leu Pro Glu Phe Ile Phe Tyr Glu Thr Glu Glu
165 170 175

Leu Phe Glu Glu Thr Leu Cys Ser Ala Leu Tyr Pro Glu Asp Thr Val
180 185 190

Tyr Ser Trp Arg His Phe His Thr Leu Arg Met Thr Ile Phe Cys Leu
195 200 205

Val Leu Pro Leu Leu Val Met Ala Ile Cys Tyr Thr Gly Ile Ile Lys
210 215 220

Thr Leu Leu Arg Cys Pro Ser Lys Lys Tyr Lys Ala Ile Arg Leu
225 230 235 240

Ile Phe Val Ile Met Ala Val Phe Phe Ile Phe Trp Thr Pro Tyr Asn
245 250 255

Val Ala Ile Leu Leu Ser Ser Tyr Gln Ser Ile Leu Phe Gly Asn Asp
260 265 270

Cys Glu Arg Ser Lys His Leu Asp Leu Val Met Leu Val Thr Glu Val
275 280 285

Ile Ala Tyr Ser His Cys Cys Met Asn Pro Val Ile Tyr Ala Phe Val
290 295 300

Gly Glu Arg Phe Arg Lys Tyr Leu Arg His Phe Phe His Arg His Leu
305 310 315 320

Leu Met His Leu Gly Arg Tyr Ile Pro Phe Leu Pro Ser Glu Lys Leu
325 330 335

Glu Arg Thr Ser Ser Val Ser Pro Ser Thr Ala Glu Pro Glu Leu Ser
340 345 350

Ile Val Phe
355

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION: /= "V28degf2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GACGGATCCA TYGAYAGRAT CCTGGCYATY GTCC

34

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION: /= "V28degr2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCTAAGCTTT TRTAGGGDGT CCAYAAGAGY AA

32

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION: /= "88c-r4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GATAAGCCTC ACAGCCCTGT G

21

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION: /= "88c-rlb"

- 53 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCTAAGCTTG ATGACTATCT TTAATGTC

28

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: /= "88-2B-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCCTCTAGAC TAAAACACAA TAGAGAG

27

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: /= "88-2B-5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCTAAGCTTA TCACAGGGAG AAGTGAAATG

30

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: /= "88-2B-f1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGTGCTAGCA GCTTCCCTG

20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- 54 -

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: /= "88-2B-r1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CAGCAGCGTT TTGATGATTC

20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: /= "88C-f1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TGTGTTTGCT TAAAAAGCC

19

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: /= "88C-r3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TAAGCCTCAC AGCCCTG

17

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: /= "CCCKR1(2)-5■ Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGTAAGCTTA GAGAAGCCGG GATGGGAA

28

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iv) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: /= "CCCKR-3■ Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCCTCTAGAG TCAGAGACCA GCAGA

25

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACAAGCTTC ACAGGGTGGA ACAAGATG

28

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTCTCTAGAC CACTTGAGTC CGTGTCA

27

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1059 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATG GAC TAT CAA GTG TCA AGT CCA ACC TAT GAC ATC GAT TAT TAT ACA Met Asp Tyr Gln Val Ser Ser Pro Thr Tyr Asp Ile Asp Tyr Tyr Thr 1 5 10 15	48
TCG GAA CCC TGC CAA AAA ATC AAT GTG AAA CAA ATC GCA GCC CGC CTC Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu 20 25 30	96
CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT GGT TTT GTG GGC AAC Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn 35 40 45	144
ATA CTG GTC GTC CTC ATC CTG ATA AAC TGC AAA AGG CTG AAA AGC ATG Ile Leu Val Val Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met 50 55 60	192
ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT GAC CTG CTT TTC CTT Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu 65 70 75 80	240
CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCT GCC CAG TGG GAC TTT Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe 85 90 95	288
GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe 100 105 110	336
TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu 115 120 125	384
GCT ATC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACA GTC ACC TTT Ala Ile Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe 130 135 140	432
GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GCT GTG TTT GCC TCT Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser 145 150 155 160	480
CTC CCA GGA ATC ATC TTT ACC AGA TCT CAG AGA GAA GGT CTT CAT TAC Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Arg Glu Gly Leu His Tyr 165 170 175	528
ACC TGC AGC TCT CAT TTT CCA TAC AGT CAG TAT CAA TTC TGG AAG AAT Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn 180 185 190	576
TTT CAG ACA TTA AAG ATG GTC ATC TTG GGG CTG GTC CTG CCG CTG CTT Phe Gln Thr Leu Lys Met Val Ile Leu Gly Leu Val Leu Pro Leu Leu 195 200 205	624
GTC ATG GTC ATC TGC TAC TCG GGA ATC CTG AAA ACT CTG CTT CGG TGT Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys 210 215 220	672
CGA AAC GAG AAG AAG AGG CAC AGG GCT GTG AGG CTT ATC TTC ACC ATC Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile 225 230 235 240	720
ATG ATT GTT TAT TTT CTC TTG TGG GCT CCC TAC AAC ATT GTC CTT CTC Met Ile Val Tyr Phe Leu Leu Trp Ala Pro Tyr Asn Ile Val Leu Leu 245 250 255	768
CTG AAC ACC TTC CAG GAA TTC TTT GGC CTG AAT AAT TGC AGT AGC TCT Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser 260 265 270	816

AAC AGG TTG GAC CAA GCC ATG CAG GTG ACA GAG ACT CTT GGG ATG ACA Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr 275 280 285	864
CAC TGC TGC ATC AAC CCC ATC ATC TAT GCC TTT GTC GGG GAG AAG TTC His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe 290 295 300	912
AGA AAC TAC CTC TTA GTC TTC TTC CAA AAG CAC ATT GCC AAA CGC TTC Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe 305 310 315 320	960
TGC AAA TGC TGT TCC ATT TTC CAG CAA GAG GCT CCC GAG CGA GCA AGT Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser 325 330 335	1008
TCA GTT TAC ACC CGA TCC ACT GGG GAG CAG GAA ATA TCT GTG GGC TTG Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu 340 345 350	1056
TGA	1059

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Asp Tyr Gln Val Ser Ser Pro Thr Tyr Asp Ile Asp Tyr Tyr Thr
1 5 10 15

Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
20 25 30

Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
35 40 45

Ile Leu Val Val Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
50 55 60

Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu
65 70 75 80

Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
85 90 95

Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
100 105 110

Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
115 120 125

Ala Ile Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
130 135 140

Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
145 150 155 160

Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Arg Glu Gly Leu His Tyr
165 170 175

Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
180 185 190

Phe Gln Thr Leu Lys Met Val Ile Leu Gly Leu Val Leu Pro Leu Leu
195 200 205

Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
210 215 220

Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
225 230 235 240

Met Ile Val Tyr Phe Leu Leu Trp Ala Pro Tyr Asn Ile Val Leu Leu
245 250 255

Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser
260 265 270

Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
275 280 285

His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
290 295 300

Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
305 310 315 320

Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
325 330 335

Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu
340 345 350